

SEQUENCE LISTING



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Urlaub, Henning  
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<120> RNA-Interference by Single-Stranded RNA Molecules

<130> 2923-673

<140> 10/520,470

<141> 2005-01-07

<150> EP 02015532.1

<151> 2002-07-10

<150> EP 02018906.4

<151> 2002-08-23

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<151> 2003-07-10

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<170> PatentIn version 3.3

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Thr Glu Tyr Val Ala Glu Ser Phe Leu Asn Cys Leu Arg Arg  
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Tyr Asn His Asp Leu Pro Ala Arg Ile Ile Val Tyr Arg  
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target RNA

<400> 37

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strand of siRNA duplex

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cguacgcgga auacuucgau u

21

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strand of siRNA duplex

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Val Leu Gln Pro Pro Ser Ile Leu Tyr Gly Gly Arg  
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Gln Glu Ile Ile Gln Asp Leu Ala Ala Met Val Arg  
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His Leu Pro Ser Met Arg Tyr Thr Pro Val Gly Arg  
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Lys Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Arg  
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Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro Met Phe Arg  
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Asp Lys Val Glu Leu Glu Val Thr Leu Pro Gly Glu Gly Lys  
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Asp Ala Gly Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys  
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Thr Gln Ile Phe Gly Asp Arg Lys Pro Val Phe Asp Gly Arg  
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Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Lys  
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Asp Tyr Gln Pro Gly Ile Thr Phe Ile Val Val Gln Lys Arg  
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Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Lys Leu Met Arg  
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Ser Gly Gln Ser Asn Gly Arg  
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1 5 10

<210> 60  
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<210> 67  
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Arg

<210> 68  
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Leu Gln Gln Val Phe Gln Ala Pro Arg Arg Pro Gly Ile Gly Thr Val  
20 25 30

Gly Lys Pro Ile Lys Leu Leu Ala Asn Tyr Phe Glu Val Asp Ile Pro  
35 40 45

Lys Ile Asp Val Tyr His Tyr Glu Val Asp Ile Lys Pro Asp Lys Cys  
50 55 60

Pro Arg Arg Val Asn Arg Glu Val Val Glu Tyr Met Val Gln His Phe  
65 70 75 80

Lys Pro Gln Ile Phe Gly Asp Arg Lys Pro Val Tyr Asp Gly Lys Lys  
85 90 95

Asn Ile Tyr Thr Val Thr Ala Leu Pro Ile Gly Asn Glu Arg Val Asp

100

105

110

Phe Glu Val Thr Ile Pro Gly Glu Gly Lys Asp Arg Ile Phe Lys Val  
 115 120 125

Ser Ile Lys Trp Leu Ala Ile Val Ser Trp Arg Met Leu His Glu Ala  
 130 135 140

Leu Val Ser Gly Gln Ile Pro Val Pro Leu Glu Ser Val Gln Ala Leu  
 145 150 155 160

Asp Val Ala Met Arg His Leu Ala Ser Met Arg Tyr Thr Pro Val Gly  
 165 170 175

Arg Ser Phe Phe Ser Pro Pro Glu Gly Tyr Tyr His Pro Leu Gly Gly  
 180 185 190

Gly Arg Glu Val Trp Phe Gly Phe His Gln Ser Val Arg Pro Ala Met  
 195 200 205

Trp Lys Met Met Leu Asn Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys  
 210 215 220

Ala Gln Pro Val Ile Glu Phe Met Cys Glu Val Leu Asp Ile Arg Asn  
 225 230 235 240

Ile Asp Glu Gln Pro Lys Pro Leu Thr Asp Ser Gln Arg Val Arg Phe  
 245 250 255

Thr Lys Glu Ile Lys Gly Leu Lys Val Glu Val Thr His Cys Gly Gln  
 260 265 270

Met Lys Arg Lys Tyr Arg Val Cys Asn Val Thr Arg Arg Pro Ala Ser  
 275 280 285

His Gln Thr Phe Pro Leu Gln Leu Glu Ser Gly Gln Thr Val Glu Cys  
 290 295 300

Thr Val Ala Gln Tyr Phe Lys Gln Lys Tyr Asn Leu Gln Leu Lys Tyr  
 305 310 315 320



Pro His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys His Thr Tyr  
 325 330 335

Leu Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg Cys Ile Lys  
 340 345 350

Lys Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Lys Ala Thr Ala Arg  
 355 360 365

Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Arg Leu Met Lys Asn Ala  
 370 375 380

Ser Tyr Asn Leu Asp Pro Tyr Ile Gln Glu Phe Gly Ile Lys Val Lys  
 385 390 395 400

Asp Asp Met Thr Glu Val Thr Gly Arg Val Leu Pro Ala Pro Ile Leu  
 405 410 415

Gln Tyr Gly Gly Arg Asn Arg Ala Ile Ala Thr Pro Asn Gln Gly Val  
 420 425 430

Trp Asp Met Arg Gly Lys Gln Phe Tyr Asn Gly Ile Glu Ile Lys Val  
 435 440 445

Trp Ala Ile Ala Cys Phe Ala Pro Gln Lys Gln Cys Arg Glu Glu Val  
 450 455 460

Leu Lys Asn Phe Thr Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly  
 465 470 475 480

Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala  
 485 490 495

Asp Ser Val Glu Pro Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly  
 500 505 510

Leu Gln Leu Ile Ile Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala  
 515 520 525

Glu Val Lys Arg Val Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys  
 530 535 540

Val Gln Val Lys Asn Val Val Lys Thr Ser Pro Gln Thr Leu Ser Asn  
545 550 555 560

Leu Cys Leu Lys Ile Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu  
565 570 575

Val Pro His Gln Arg Ser Ala Val Phe Gln Gln Pro Val Ile Phe Leu  
580 585 590

Gly Ala Asp Val Thr His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser  
595 600 605

Ile Thr Ala Val Val Gly Ser Met Asp Ala His Pro Ser Arg Tyr Cys  
610 615 620

Ala Thr Val Arg Val Gln Arg Pro Arg Gln Glu Ile Ile Glu Asp Leu  
625 630 635 640

Ser Tyr Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys Ser Thr Arg  
645 650 655

Phe Lys Pro Thr Arg Ile Ile Phe Tyr Arg Asp Gly Val Pro Glu Gly  
660 665 670

Gln Leu Pro Gln Ile Leu His Tyr Glu Leu Leu Ala Ile Arg Asp Ala  
675 680 685

Cys Ile Lys Leu Glu Lys Asp Tyr Gln Pro Gly Ile Thr Tyr Ile Val  
690 695 700

Val Gln Lys Arg His His Thr Arg Leu Phe Cys Ala Asp Lys Asn Glu  
705 710 715 720

Arg Ile Gly Lys Ser Gly Asn Ile Pro Ala Gly Thr Thr Val Asp Thr  
725 730 735

Asn Ile Thr His Pro Phe Glu Phe Asp Phe Tyr Leu Cys Ser His Ala  
740 745 750

Gly Ile Gln Gly Thr Ser Arg Pro Ser His Tyr Tyr Val Leu Trp Asp  
755 760 765

Asp Asn Arg Phe Thr Ala Asp Glu Leu Gln Ile Leu Thr Tyr Gln Leu  
 770 775 780

Cys His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro  
 785 790 795 800

Ala Tyr Tyr Ala Arg Leu Val Ala Phe Arg Ala Arg Tyr His Leu Val  
 805 810 815

Asp Lys Glu His Asp Ser Gly Glu Gly Ser His Ile Ser Gly Gln Ser  
 820 825 830

Asn Gly Arg Asp Pro Gln Ala Leu Ala Lys Ala Val Gln Val His Gln  
 835 840 845

Asp Thr Leu Arg Thr Met Tyr Phe Ala  
 850 855

<210> 69  
 <211> 860  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <223> eIF2C2, predicted protein sequence

<400> 69

Met Gly Val Leu Ser Ala Ile Pro Ala Leu Ala Pro Pro Ala Pro Pro  
 1 5 10 15

Pro Pro Ile Gln Gly Tyr Ala Phe Lys Pro Pro Pro Arg Pro Asp Phe  
 20 25 30

Gly Thr Ser Gly Arg Thr Ile Lys Leu Gln Ala Asn Phe Phe Glu Met  
 35 40 45

Asp Ile Pro Lys Ile Asp Ile Tyr His Tyr Glu Leu Asp Ile Lys Pro  
 50 55 60

Glu Lys Cys Pro Arg Arg Val Asn Arg Glu Ile Val Glu His Met Val

65

70

75

80

Gln His Phe Lys Thr Gln Ile Phe Gly Asp Arg Lys Pro Val Phe Asp  
85 90 95

Gly Arg Lys Asn Leu Tyr Thr Ala Met Pro Leu Pro Ile Gly Arg Asp  
100 105 110

Lys Val Glu Leu Glu Val Thr Leu Pro Gly Glu Gly Lys Asp Arg Ile  
115 120 125

Phe Lys Val Ser Ile Lys Trp Val Ser Cys Val Ser Leu Gln Ala Leu  
130 135 140

His Asp Ala Leu Ser Gly Arg Leu Pro Ser Val Pro Phe Glu Thr Ile  
145 150 155 160

Gln Ala Leu Asp Val Val Met Arg His Leu Pro Ser Met Arg Tyr Thr  
165 170 175

Pro Val Gly Arg Ser Phe Phe Thr Ala Ser Glu Gly Cys Ser Asn Pro  
180 185 190

Leu Gly Gly Gly Arg Glu Val Trp Phe Gly Phe His Gln Ser Val Arg  
195 200 205

Pro Ser Leu Trp Lys Met Met Leu Asn Ile Asp Val Ser Ala Thr Ala  
210 215 220

Phe Tyr Lys Ala Gln Pro Val Ile Glu Phe Val Cys Glu Val Leu Asp  
225 230 235 240

Phe Lys Ser Ile Glu Glu Gln Gln Lys Pro Leu Thr Asp Ser Gln Arg  
245 250 255

Val Lys Phe Thr Lys Glu Ile Lys Gly Leu Lys Val Glu Ile Thr His  
260 265 270

Cys Gly Gln Met Lys Arg Lys Tyr Arg Val Cys Asn Val Thr Arg Arg  
275 280 285

Pro Ala Ser His Gln Thr Phe Pro Leu Gln Gln Glu Ser Gly Gln Thr  
 290 295 300

Val Glu Cys Thr Val Ala Gln Tyr Phe Lys Asp Arg His Lys Leu Val  
 305 310 315 320

Leu Arg Tyr Pro His Leu Pro Cys Leu Gln Val Gly Gln Glu Gln Lys  
 325 330 335

His Thr Tyr Leu Pro Leu Glu Val Cys Asn Ile Val Ala Gly Gln Arg  
 340 345 350

Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr Ser Thr Met Ile Arg Ala  
 355 360 365

Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu Glu Ile Ser Lys Leu Met  
 370 375 380

Arg Ser Ala Ser Phe Asn Thr Asp Pro Tyr Val Arg Glu Phe Gly Ile  
 385 390 395 400

Met Val Lys Asp Glu Met Thr Asp Val Thr Gly Arg Val Leu Gln Pro  
 405 410 415

Pro Ser Ile Leu Tyr Gly Gly Arg Asn Lys Ala Ile Ala Thr Pro Val  
 420 425 430

Gln Gly Val Trp Asp Met Arg Asn Lys Gln Phe His Thr Gly Ile Glu  
 435 440 445

Ile Lys Val Trp Ala Ile Ala Cys Phe Ala Pro Gln Arg Gln Cys Thr  
 450 455 460

Glu Val His Leu Lys Ser Phe Thr Glu Gln Leu Arg Lys Ile Ser Arg  
 465 470 475 480

Asp Ala Gly Met Pro Ile Gln Gly Gln Pro Cys Phe Cys Lys Tyr Ala  
 485 490 495

Gln Gly Ala Asp Ser Val Glu Pro Met Phe Arg His Leu Lys Asn Thr  
 500 505 510

Tyr Ala Gly Leu Gln Leu Val Val Val Ile Leu Pro Gly Lys Thr Pro  
515 520 525

Val Tyr Ala Glu Val Lys Arg Val Gly Asp Thr Val Leu Gly Met Ala  
530 535 540

Thr Gln Cys Val Gln Met Lys Asn Val Gln Arg Thr Thr Pro Gln Thr  
545 550 555 560

Leu Ser Asn Leu Cys Leu Lys Ile Asn Val Lys Leu Gly Gly Val Asn  
565 570 575

Asn Ile Leu Leu Pro Gln Gly Arg Pro Pro Val Phe Gln Gln Pro Val  
580 585 590

Ile Phe Leu Gly Ala Asp Val Thr His Pro Pro Ala Gly Asp Gly Lys  
595 600 605

Lys Pro Ser Ile Ala Ala Val Val Gly Ser Met Asp Ala His Pro Asn  
610 615 620

Arg Tyr Cys Ala Thr Val Arg Val Gln Gln His Arg Gln Glu Ile Ile  
625 630 635 640

Gln Asp Leu Ala Ala Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys  
645 650 655

Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile Phe Tyr Arg Asp Gly Val  
660 665 670

Ser Glu Gly Gln Phe Gln Gln Val Leu His His Glu Leu Leu Ala Ile  
675 680 685

Arg Glu Ala Cys Ile Lys Leu Glu Lys Asp Tyr Gln Pro Gly Ile Thr  
690 695 700

Phe Ile Val Val Gln Lys Arg His His Thr Arg Leu Phe Cys Thr Asp  
705 710 715 720

Lys Asn Glu Arg Val Gly Lys Ser Gly Asn Ile Pro Ala Gly Thr Thr  
725 730 735

Val Asp Thr Lys Ile Thr His Pro Thr Glu Phe Asp Phe Tyr Leu Cys  
740 745 750

Ser His Ala Gly Ile Gln Gly Thr Ser Arg Pro Ser His Tyr His Val  
755 760 765

Leu Trp Asp Asp Asn Arg Phe Ser Ser Asp Glu Leu Gln Ile Leu Thr  
770 775 780

Tyr Gln Leu Cys His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile  
785 790 795 800

Pro Ala Pro Ala Tyr Tyr Ala His Leu Val Ala Phe Arg Ala Arg Tyr  
805 810 815

His Leu Val Asp Lys Glu His Asp Ser Ala Glu Gly Ser His Thr Ser  
820 825 830

Gly Gln Ser Asn Gly Arg Asp His Gln Ala Leu Ala Lys Ala Val Gln  
835 840 845

Val His Gln Asp Thr Leu Arg Thr Met Tyr Phe Ala  
850 855 860

<210> 70  
<211> 924  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<223> eIF2C3, predicted protein sequence

<400> 70

Ser Arg Ser Arg Val Pro Val Pro Gly Pro Gly Ala Ala Ala Ala Pro  
1 5 10 15

Cys Pro Ala Pro Ala Ser Pro Arg Arg His Pro Ser Ala Asn Ile Pro  
20 25 30

Glu Ile Lys Arg Tyr Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly

35

40

45

Ala Gly Gly Ala Gly Asp Arg Gly Glu Ala Ala Pro Ala Ala Ala Met  
50 55 60

Glu Ala Leu Gly Pro Gly Pro Pro Ala Ser Leu Phe Gln Pro Pro Arg  
65 70 75 80

Arg Pro Gly Leu Gly Thr Val Gly Lys Pro Ile Arg Leu Leu Ala Asn  
85 90 95

His Phe Gln Val Gln Ile Pro Lys Ile Asp Val Tyr His Tyr Asp Val  
100 105 110

Asp Ile Lys Pro Glu Lys Arg Pro Arg Arg Val Asn Arg Glu Val Val  
115 120 125

Asp Thr Met Val Arg His Phe Lys Met Gln Ile Phe Gly Asp Arg Gln  
130 135 140

Pro Gly Tyr Asp Gly Lys Arg Asn Met Tyr Thr Ala His Pro Leu Pro  
145 150 155 160

Ile Gly Arg Asp Arg Val Asp Met Glu Val Thr Leu Pro Gly Glu Gly  
165 170 175

Lys Asp Gln Thr Phe Lys Val Ser Val Gln Trp Val Ser Val Val Ser  
180 185 190

Leu Gln Leu Leu Leu Glu Ala Leu Ala Gly His Leu Asn Glu Val Pro  
195 200 205

Asp Asp Ser Val Gln Ala Leu Asp Val Ile Thr Arg His Leu Pro Ser  
210 215 220

Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Ser Pro Pro Glu Gly  
225 230 235 240

Tyr Tyr His Pro Leu Gly Gly Gly Arg Glu Val Trp Phe Gly Phe His  
245 250 255



Gln Ser Val Arg Pro Ala Met Trp Asn Met Met Leu Asn Ile Asp Val  
 260 265 270

Ser Ala Thr Ala Phe Tyr Arg Ala Gln Pro Ile Ile Glu Phe Met Cys  
 275 280 285

Glu Val Leu Asp Ile Gln Asn Ile Asn Glu Gln Thr Lys Pro Leu Thr  
 290 295 300

Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Arg Gly Leu Lys Val  
 305 310 315 320

Glu Val Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg Val Cys Asn  
 325 330 335

Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu Gln Leu Glu  
 340 345 350

Asn Gly Gln Ala Met Glu Cys Thr Val Ala Gln Tyr Phe Lys Gln Lys  
 355 360 365

Tyr Ser Leu Gln Leu Lys Tyr Pro His Leu Pro Cys Leu Gln Val Gly  
 370 375 380

Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys Asn Ile Val  
 385 390 395 400

Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr Ser Thr  
 405 410 415

Met Ile Lys Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu Glu Ile  
 420 425 430

Ser Arg Leu Val Lys Ser Asn Ser Met Val Gly Gly Pro Asp Pro Tyr  
 435 440 445

Leu Lys Glu Phe Gly Ile Val Val His Asn Glu Met Thr Glu Leu Thr  
 450 455 460

Gly Arg Val Leu Pro Ala Pro Met Leu Gln Tyr Gly Gly Arg Asn Lys  
 465 470 475 480

Thr	Val	Ala	Thr	Pro	Asn	Gln	Gly	Val	Trp	Asp	Met	Arg	Gly	Lys	Gln	485	490	495
Phe	Tyr	Ala	Gly	Ile	Glu	Ile	Lys	Val	Trp	Ala	Val	Ala	Cys	Phe	Ala	500	505	510
Pro	Gln	Lys	Gln	Cys	Arg	Glu	Asp	Leu	Leu	Lys	Ser	Phe	Thr	Asp	Gln	515	520	525
Leu	Arg	Lys	Ile	Ser	Lys	Asp	Ala	Gly	Met	Pro	Ile	Gln	Gly	Gln	Pro	530	535	540
Cys	Phe	Cys	Lys	Tyr	Ala	Gln	Gly	Ala	Asp	Ser	Val	Glu	Pro	Met	Phe	545	550	555
Lys	His	Leu	Lys	Met	Thr	Tyr	Val	Gly	Leu	Gln	Leu	Ile	Val	Val	Ile	565	570	575
Leu	Pro	Gly	Lys	Thr	Pro	Val	Tyr	Ala	Glu	Val	Lys	Arg	Val	Gly	Asp	580	585	590
Thr	Leu	Leu	Gly	Met	Ala	Thr	Gln	Cys	Val	Gln	Val	Lys	Asn	Val	Val	595	600	605
Lys	Thr	Ser	Pro	Gln	Thr	Leu	Ser	Asn	Leu	Cys	Leu	Lys	Ile	Asn	Ala	610	615	620
Lys	Leu	Gly	Gly	Ile	Asn	Asn	Val	Leu	Val	Pro	His	Gln	Arg	Pro	Ser	625	630	635
Val	Phe	Gln	Gln	Pro	Val	Ile	Phe	Leu	Gly	Ala	Asp	Val	Thr	His	Pro	645	650	655
Pro	Ala	Gly	Asp	Gly	Lys	Lys	Pro	Ser	Ile	Ala	Ala	Val	Val	Gly	Ser	660	665	670
Met	Asp	Gly	His	Pro	Ser	Arg	Tyr	Cys	Ala	Thr	Val	Arg	Val	Gln	Thr	675	680	685
Ser	Arg	Gln	Glu	Ile	Ser	Gln	Glu	Leu	Leu	Tyr	Ser	Gln	Glu	Val	Ile	690	695	700

Gln Asp Leu Thr Asn Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys  
705 710 715 720

Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile Tyr Tyr Arg Gly Gly Val  
725 730 735

Ser Glu Gly Gln Met Lys Gln Val Ala Trp Pro Glu Leu Ile Ala Ile  
740 745 750

Arg Lys Ala Cys Ile Ser Leu Glu Glu Asp Tyr Arg Pro Gly Ile Thr  
755 760 765

Tyr Ile Val Val Gln Lys Arg His His Thr Arg Leu Phe Cys Ala Asp  
770 775 780

Lys Thr Glu Arg Val Gly Lys Ser Gly Asn Val Pro Ala Gly Thr Thr  
785 790 795 800

Val Asp Ser Thr Ile Thr His Pro Ser Glu Phe Asp Phe Tyr Leu Cys  
805 810 815

Ser His Ala Gly Ile Gln Gly Thr Ser Arg Pro Ser His Tyr Gln Val  
820 825 830

Leu Trp Asp Asp Asn Cys Phe Thr Ala Asp Glu Leu Gln Leu Leu Thr  
835 840 845

Tyr Gln Leu Cys His Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile  
850 855 860

Pro Ala Pro Ala Tyr Tyr Ala Arg Leu Val Ala Phe Arg Ala Arg Tyr  
865 870 875 880

His Leu Val Asp Lys Asp His Asp Ser Ala Glu Gly Ser His Val Ser  
885 890 895

Gly Gln Ser Asn Gly Arg Asp Pro Gln Ala Leu Ala Lys Ala Val Gln  
900 905 910

Ile His His Asp Thr Gln His Thr Met Tyr Phe Ala

<210> 71  
 <211> 855  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <223> eIF2C4, predicted protein sequence

<400> 71

Ala Gly Pro Ala Gly Ala Gln Pro Leu Leu Met Val Pro Arg Arg Pro  
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Gly Tyr Gly Thr Met Gly Lys Pro Ile Lys Leu Leu Ala Asn Cys Phe  
 20 25 30

Gln Val Glu Ile Pro Lys Ile Asp Val Tyr Leu Tyr Glu Val Asp Ile  
 35 40 45

Lys Pro Asp Lys Cys Pro Arg Arg Val Asn Arg Glu Val Val Asp Ser  
 50 55 60

Met Val Gln His Phe Lys Val Thr Ile Phe Gly Asp Arg Arg Pro Val  
 65 70 75 80

Tyr Asp Gly Lys Arg Ser Leu Tyr Thr Ala Asn Pro Leu Pro Val Ala  
 85 90 95

Thr Thr Gly Val Asp Leu Asp Val Thr Leu Pro Gly Glu Gly Gly Lys  
 100 105 110

Asp Arg Pro Phe Lys Val Ser Ile Lys Phe Val Ser Arg Val Ser Trp  
 115 120 125

His Leu Leu His Glu Val Leu Thr Gly Arg Thr Leu Pro Glu Pro Leu  
 130 135 140

Glu Leu Asp Lys Pro Ile Ser Thr Asn Pro Val His Ala Val Asp Val  
 145 150 155 160

Val	Leu	Arg	His	Leu	Pro	Ser	Met	Lys	Tyr	Thr	Pro	Val	Gly	Arg	Ser	165	170	175
Phe	Phe	Ser	Ala	Pro	Glu	Gly	Tyr	Asp	His	Pro	Leu	Gly	Gly	Gly	Arg	180	185	190
Glu	Val	Trp	Phe	Gly	Phe	His	Gln	Ser	Val	Arg	Pro	Ala	Met	Trp	Lys	195	200	205
Met	Met	Leu	Asn	Ile	Asp	Val	Ser	Ala	Thr	Ala	Phe	Tyr	Lys	Ala	Gln	210	215	220
Pro	Val	Ile	Gln	Phe	Met	Cys	Glu	Val	Leu	Asp	Ile	His	Asn	Ile	Asp	225	230	235
Glu	Gln	Pro	Arg	Pro	Leu	Thr	Asp	Ser	His	Arg	Val	Lys	Phe	Thr	Lys	245	250	255
Glu	Ile	Lys	Gly	Leu	Lys	Val	Glu	Val	Thr	His	Cys	Gly	Thr	Met	Arg	260	265	270
Arg	Lys	Tyr	Arg	Val	Cys	Asn	Val	Thr	Arg	Arg	Pro	Ala	Ser	His	Gln	275	280	285
Thr	Phe	Pro	Leu	Gln	Leu	Glu	Asn	Gly	Gln	Thr	Val	Glu	Arg	Thr	Val	290	295	300
Ala	Gln	Tyr	Phe	Arg	Glu	Lys	Tyr	Thr	Leu	Gln	Leu	Lys	Tyr	Pro	His	305	310	315
Leu	Pro	Cys	Leu	Gln	Val	Gly	Gln	Glu	Gln	Lys	His	Thr	Tyr	Leu	Pro	325	330	335
Leu	Glu	Val	Cys	Asn	Ile	Val	Ala	Gly	Gln	Arg	Cys	Ile	Lys	Lys	Leu	340	345	350
Thr	Asp	Asn	Gln	Thr	Ser	Thr	Met	Ile	Lys	Ala	Thr	Ala	Arg	Ser	Ala	355	360	365
Pro	Asp	Arg	Gln	Glu	Glu	Ile	Ser	Arg	Leu	Val	Arg	Ser	Ala	Asn	Tyr	370	375	380

Glu Thr Asp Pro Phe Val Gln Glu Phe Gln Phe Lys Val Arg Asp Glu  
 385 390 395 400

Met Ala His Val Thr Gly Arg Val Leu Pro Ala Pro Met Leu Gln Tyr  
 405 410 415

Gly Gly Arg Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp  
 420 425 430

Met Arg Gly Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala  
 435 440 445

Ile Ala Cys Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys  
 450 455 460

Gly Phe Thr Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro  
 465 470 475 480

Ile Gln Gly Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser  
 485 490 495

Val Glu Pro Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln  
 500 505 510

Leu Ile Ile Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val  
 515 520 525

Lys Arg Val Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln  
 530 535 540

Val Lys Asn Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys  
 545 550 555 560

Leu Lys Ile Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro  
 565 570 575

His Gln Arg Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala  
 580 585 590

Asp Val Thr His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala  
 595 600 605

Ala Val Val Gly Ser Met Asp Ala His Pro Ser Arg Tyr Cys Ala Thr  
 610 615 620

Val Arg Val Gln Arg Pro Arg Gln Glu Ile Ile Gln Asp Leu Ala Ser  
 625 630 635 640

Met Val Arg Glu Leu Leu Ile Gln Phe Tyr Lys Ser Thr Arg Phe Lys  
 645 650 655

Pro Thr Arg Ile Ile Phe Tyr Arg Asp Gly Val Ser Glu Gly Gln Phe  
 660 665 670

Arg Gln Val Leu Tyr Tyr Glu Leu Leu Ala Ile Arg Glu Ala Cys Ile  
 675 680 685

Ser Leu Glu Lys Asp Tyr Gln Pro Gly Ile Thr Tyr Ile Val Val Gln  
 690 695 700

Lys Arg His His Thr Arg Leu Phe Cys Ala Asp Arg Thr Glu Arg Val  
 705 710 715 720

Gly Arg Ser Gly Asn Ile Pro Ala Gly Thr Thr Val Asp Thr Asp Ile  
 725 730 735

Thr His Pro Tyr Glu Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile  
 740 745 750

Gln Gly Thr Ser Arg Pro Ser His Tyr His Val Leu Trp Asp Asp Asn  
 755 760 765

Cys Phe Thr Ala Asp Glu Leu Gln Leu Leu Thr Tyr Gln Leu Cys His  
 770 775 780

Thr Tyr Val Arg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr  
 785 790 795 800

Tyr Ala His Leu Val Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys  
 805 810 815

Glu His Asp Ser Ala Glu Gly Ser His Val Ser Gly Gln Ser Asn Gly

820

825

830

Arg Asp Pro Gln Ala Leu Ala Lys Ala Val Gln Ile His Gln Asp Thr  
 835 840 845

Leu Arg Thr Met Tyr Phe Ala  
 850 855

<210> 72  
 <211> 764  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <223> HILI, predicted protein sequence

<400> 72

Ile Ser Ser Gly Asp Ala Gly Ser Thr Phe Met Glu Arg Gly Val Lys  
 1 5 10 15

Asn Lys Gln Asp Phe Met Asp Leu Ser Ile Cys Thr Arg Glu Lys Leu  
 20 25 30

Ala His Val Arg Asn Cys Lys Thr Gly Ser Ser Gly Ile Pro Val Lys  
 35 40 45

Leu Val Thr Asn Leu Phe Asn Leu Asp Phe Pro Gln Asp Trp Gln Leu  
 50 55 60

Tyr Gln Tyr His Val Thr Tyr Ile Pro Asp Leu Ala Ser Arg Arg Leu  
 65 70 75 80

Arg Ile Ala Leu Leu Tyr Ser His Ser Glu Leu Ser Asn Lys Ala Lys  
 85 90 95

Ala Phe Asp Gly Ala Ile Leu Phe Leu Ser Gln Lys Leu Glu Glu Lys  
 100 105 110

Val Thr Glu Leu Ser Ser Glu Thr Gln Arg Gly Glu Thr Ile Lys Met  
 115 120 125



Thr	Ile	Thr	Leu	Lys	Arg	Glu	Leu	Pro	Ser	Ser	Ser	Pro	Val	Cys	Ile
130						135					140				
Gln	Val	Phe	Asn	Ile	Ile	Phe	Arg	Lys	Ile	Leu	Lys	Lys	Leu	Ser	Met
145					150					155					160
Tyr	Gln	Ile	Gly	Arg	Asn	Phe	Tyr	Asn	Pro	Ser	Glu	Pro	Met	Glu	Ile
				165					170					175	
Pro	Gln	His	Lys	Leu	Ser	Leu	Trp	Pro	Gly	Phe	Ala	Ile	Ser	Val	Ser
			180					185					190		
Tyr	Phe	Glu	Arg	Lys	Leu	Leu	Phe	Ser	Ala	Asp	Val	Ser	Tyr	Lys	Val
		195					200					205			
Leu	Arg	Asn	Glu	Thr	Val	Leu	Glu	Phe	Met	Thr	Ala	Leu	Cys	Gln	Arg
	210					215					220				
Thr	Gly	Leu	Ser	Cys	Phe	Thr	Gln	Thr	Cys	Glu	Lys	Gln	Leu	Ile	Gly
225					230					235					240
Leu	Ile	Val	Leu	Thr	Arg	Tyr	Asn	Asn	Arg	Thr	Tyr	Ser	Ile	Asp	Asp
				245					250					255	
Ile	Asp	Trp	Ser	Val	Lys	Pro	Thr	His	Thr	Phe	Gln	Lys	Arg	Asp	Gly
			260					265					270		
Thr	Glu	Ile	Thr	Tyr	Val	Asp	Tyr	Tyr	Lys	Gln	Gln	Tyr	Asp	Ile	Thr
		275					280					285			
Val	Ser	Asp	Leu	Asn	Gln	Pro	Met	Leu	Val	Ser	Leu	Leu	Lys	Lys	Lys
	290					295					300				
Arg	Asn	Asp	Asn	Ser	Glu	Ala	Gln	Leu	Ala	His	Leu	Ile	Pro	Glu	Leu
305					310					315					320
Cys	Phe	Leu	Thr	Gly	Leu	Thr	Asp	Gln	Ala	Thr	Ser	Asp	Phe	Gln	Leu
				325					330					335	
Met	Lys	Ala	Val	Ala	Glu	Lys	Thr	Arg	Leu	Ser	Pro	Ser	Gly	Arg	Gln
			340					345					350		

Gln Arg Leu Ala Arg Leu Val Asp Asn Ile Gln Arg Asn Thr Asn Ala  
 355 360 365

Arg Phe Glu Leu Glu Thr Trp Gly Leu His Phe Gly Ser Gln Ile Ser  
 370 375 380

Leu Thr Gly Arg Ile Val Pro Ser Glu Lys Ile Leu Met Gln Asp His  
 385 390 395 400

Ile Cys Gln Pro Val Ser Ala Ala Asp Trp Ser Lys Asp Ile Arg Thr  
 405 410 415

Cys Lys Ile Leu Asn Ala Gln Ser Leu Asn Thr Trp Leu Ile Leu Cys  
 420 425 430

Ser Asp Arg Thr Glu Tyr Val Ala Glu Ser Phe Leu Asn Cys Leu Arg  
 435 440 445

Arg Val Ala Gly Ser Met Gly Phe Asn Val Met Cys Ile Leu Pro Ser  
 450 455 460

Asn Gln Lys Thr Tyr Tyr Asp Ser Ile Lys Lys Tyr Leu Ser Ser Asp  
 465 470 475 480

Cys Pro Val Pro Ser Gln Cys Val Leu Ala Arg Thr Leu Asn Lys Gln  
 485 490 495

Gly Met Met Met Ser Ile Ala Thr Lys Ile Ala Met Gln Met Thr Cys  
 500 505 510

Lys Leu Gly Gly Glu Leu Trp Ala Val Glu Ile Pro Leu Lys Ser Leu  
 515 520 525

Met Val Val Gly Ile Asp Val Cys Lys Asp Ala Leu Ser Lys Asp Val  
 530 535 540

Met Val Val Gly Cys Val Ala Ser Val Asn Pro Arg Ile Thr Arg Trp  
 545 550 555 560

Phe Ser Arg Cys Ile Leu Gln Arg Thr Met Thr Asp Val Ala Asp Cys  
 565 570 575

Leu Lys Val Phe Met Thr Gly Ala Leu Asn Lys Trp Tyr Lys Tyr Asn  
580 585 590

His Asp Leu Pro Ala Arg Ile Ile Val Tyr Arg Ala Gly Val Gly Asp  
595 600 605

Gly Gln Leu Lys Thr Leu Ile Glu Tyr Glu Val Pro Gln Leu Leu Ser  
610 615 620

Ser Val Ala Glu Ser Ser Ser Asn Thr Ser Ser Arg Leu Ser Val Ile  
625 630 635 640

Val Val Arg Lys Lys Cys Met Pro Arg Phe Phe Thr Glu Met Asn Arg  
645 650 655

Thr Val Gln Asn Pro Pro Leu Gly Thr Val Val Asp Ser Glu Ala Thr  
660 665 670

Arg Asn Glu Trp Gln Tyr Asp Phe Tyr Leu Ile Ser Gln Val Ala Cys  
675 680 685

Arg Gly Thr Val Ser Pro Thr Tyr Tyr Asn Val Ile Tyr Asp Asp Asn  
690 695 700

Gly Leu Lys Pro Asp His Met Gln Arg Leu Thr Phe Lys Leu Cys His  
705 710 715 720

Leu Tyr Tyr Asn Trp Pro Gly Ile Val Ser Val Pro Ala Pro Cys Gln  
725 730 735

Tyr Ala His Lys Leu Thr Phe Leu Val Ala Gln Ser Ile His Lys Glu  
740 745 750

Pro Ser Leu Glu Leu Ala Asn His Leu Phe Tyr Leu  
755 760

<210> 73  
<211> 861  
<212> PRT  
<213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <223> HIWI, predicted protein sequence

<400> 73

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Ile	Gln	Pro	Arg	Pro	Gln	Pro	Pro	Pro	Ala	Glu	Gly	Glu	Leu	Phe	Gly	35	40	45	
Arg	Gly	Arg	Gln	Arg	Gly	Thr	Ala	Gly	Gly	Thr	Ala	Lys	Ser	Gln	Gly	50	55	60	
Leu	Gln	Ile	Ser	Ala	Gly	Phe	Gln	Glu	Leu	Ser	Leu	Ala	Glu	Arg	Gly	65	70	75	80
Gly	Arg	Arg	Arg	Asp	Phe	His	Asp	Leu	Gly	Val	Asn	Thr	Arg	Gln	Asn	85	90	95	
Leu	Asp	His	Val	Lys	Glu	Ser	Lys	Thr	Gly	Ser	Ser	Gly	Ile	Ile	Val	100	105	110	
Arg	Leu	Ser	Thr	Asn	His	Phe	Arg	Leu	Thr	Ser	Arg	Pro	Gln	Trp	Ala	115	120	125	
Leu	Tyr	Gln	Tyr	His	Ile	Asp	Tyr	Asn	Pro	Leu	Met	Glu	Ala	Arg	Arg	130	135	140	
Leu	Arg	Ser	Ala	Leu	Leu	Phe	Gln	His	Glu	Asp	Leu	Ile	Gly	Lys	Cys	145	150	155	160
His	Ala	Phe	Asp	Gly	Thr	Ile	Leu	Phe	Leu	Pro	Lys	Arg	Leu	Gln	Gln	165	170	175	
Lys	Val	Thr	Glu	Val	Phe	Ser	Lys	Thr	Arg	Asn	Gly	Glu	Asp	Val	Arg	180	185	190	

Ile	Thr	Ile	Thr	Leu	Thr	Asn	Glu	Leu	Pro	Pro	Thr	Ser	Pro	Thr	Cys
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Leu	Gln	Phe	Tyr	Asn	Ile	Ile	Phe	Arg	Arg	Leu	Leu	Lys	Ile	Met	Asn
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225					230					235					240
Ile	Pro	Ser	His	Arg	Leu	Val	Ile	Trp	Pro	Gly	Phe	Thr	Thr	Ser	Ile
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Val	Leu	Arg	Ser	Glu	Thr	Val	Leu	Asp	Phe	Met	Phe	Asn	Phe	Tyr	His
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Gln	Thr	Glu	Glu	His	Lys	Phe	Gln	Glu	Gln	Val	Ser	Lys	Glu	Leu	Ile
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Gly	Leu	Val	Val	Leu	Thr	Lys	Tyr	Asn	Asn	Lys	Thr	Tyr	Arg	Val	Asp
305					310					315					320
Asp	Ile	Asp	Trp	Asp	Gln	Asn	Pro	Lys	Ser	Thr	Phe	Lys	Lys	Ala	Asp
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Gly	Ser	Glu	Val	Ser	Phe	Leu	Glu	Tyr	Tyr	Arg	Lys	Gln	Tyr	Asn	Gln
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Glu	Ile	Thr	Asp	Leu	Lys	Gln	Pro	Val	Leu	Val	Ser	Gln	Pro	Lys	Arg
		355					360					365			
Arg	Arg	Gly	Pro	Gly	Gly	Thr	Leu	Pro	Gly	Pro	Ala	Met	Leu	Ile	Pro
	370					375					380				
Glu	Leu	Cys	Tyr	Leu	Thr	Gly	Leu	Thr	Asp	Lys	Met	Arg	Asn	Asp	Phe
385					390					395					400
Asn	Val	Met	Lys	Asp	Leu	Ala	Val	His	Thr	Arg	Leu	Thr	Pro	Glu	Gln
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Arg	Gln	Arg	Glu	Val	Gly	Arg	Leu	Ile	Asp	Tyr	Ile	His	Lys	Asn	Asp		
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Leu	Leu	Ser	Phe	Ser	Gly	Arg	Ile	Leu	Gln	Thr	Glu	Lys	Ile	His	Gln		
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Gly	Gly	Lys	Thr	Phe	Asp	Tyr	Asn	Pro	Gln	Phe	Ala	Asp	Trp	Ser	Lys		
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Glu	Thr	Arg	Gly	Ala	Pro	Leu	Ile	Ser	Val	Lys	Pro	Leu	Asp	Asn	Trp		
				485					490					495			
Leu	Leu	Ile	Tyr	Thr	Arg	Arg	Asn	Tyr	Glu	Ala	Ala	Asn	Ser	Leu	Ile		
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Gln	Asn	Leu	Phe	Lys	Val	Thr	Pro	Ala	Met	Gly	Met	Gln	Met	Arg	Lys		
		515					520					525					
Ala	Ile	Met	Ile	Glu	Val	Asp	Asp	Arg	Thr	Glu	Ala	Tyr	Leu	Arg	Val		
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Leu	Gln	Gln	Lys	Val	Thr	Ala	Asp	Thr	Gln	Ile	Val	Val	Cys	Leu	Leu		
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Ser	Ser	Asn	Arg	Lys	Asp	Lys	Tyr	Asp	Ala	Ile	Lys	Lys	Tyr	Leu	Cys		
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Thr	Asp	Cys	Pro	Thr	Pro	Ser	Gln	Cys	Val	Val	Ala	Arg	Thr	Leu	Gly		
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Lys	Gln	Gln	Thr	Val	Met	Ala	Ile	Ala	Thr	Lys	Ile	Ala	Leu	Gln	Met		
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Asn	Cys	Lys	Met	Gly	Gly	Glu	Leu	Trp	Arg	Val	Asp	Ile	Pro	Leu	Lys		
	610					615					620						
Leu	Val	Met	Ile	Val	Gly	Ile	Asp	Cys	Tyr	His	Asp	Met	Thr	Ala	Gly		
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Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr  
 645 650 655

Arg Trp Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val  
 660 665 670

Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser  
 675 680 685

Cys Asn Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val  
 690 695 700

Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe  
 705 710 715 720

Leu Asp Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr  
 725 730 735

Val Ile Val Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser  
 740 745 750

Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu  
 755 760 765

Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val  
 770 775 780

Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn  
 785 790 795 800

Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys  
 805 810 815

His Ile Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys  
 820 825 830

Gln Tyr Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg  
 835 840 845

Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu

<210> 74  
 <211> 2571  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> eIF2C1, cDNA sequence of predicted ORF

<400> 74  
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 aattactttg aggtggacat ccctaagatc gacgtgtacc actacgaggt ggacatcaag 180  
 ccggataagt gtccccgtag agtcaaccgg gaagtggtag aatacatggg ccagcatttc 240  
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 gtcacagcac tgcccattgg caacgaacgg gtgcactttg aggtgacaat ccctggggaa 360  
 gggaaggatc gaatctttaa ggtctccatc aagtggctag ccattgtgag ctggcgaatg 420  
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 atgaagaatg ccagctacaa cttagatccc tacatccagg aatttgggat caaagtgaag 1200  
 gatgacatga cggaggtgac agggcgagtg ctgccggcgc ccatcttgca gtacggcggc 1260



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<210> 75  
 <211> 2580  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> eIF2C2, cDNA sequence of predicted ORF

<400> 75

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ttacaggcca	atttcttcga	aatggacatc	cccaaaattg	acatctatca	ttatgaattg	180
gatatcaagc	cagagaagtg	cccgaggaga	gttaacaggg	aaatcgtgga	acacatggtc	240
cagcacttta	aaacacagat	ctttggggat	cggaagcccg	tgtttgacgg	caggaagaat	300
ctatacacag	ccatgcccct	tccgattggg	agggacaagg	tggagctgga	ggtcacgctg	360
ccaggagaag	gcaaggatcg	catcttcaag	gtgtccatca	agtgggtgtc	ctgcgtgagc	420
ttgcaggcgt	tacacgatgc	actttcaggg	cggctgccc	gcgtcccttt	tgagacgatc	480
caggccctgg	acgtgggtcat	gaggcacttg	ccatccatga	ggtagacccc	cgtgggcccgc	540
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 <211> 2772  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> eIF2C3, cDNA sequence of predicted ORF

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gcggcgggcg	cgcgggggcc cggagcggga ggcgccgggg accggggcgga ggcgggcccc 180
gccgcccga	tggaggcgct gggacccgga cctccggcta gcctgtttca gccacctcgt 240
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<220>  
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gtctacctct atgaggtaga tattaacca gacaagtgtc ctaggagagt gaacaggagg	180
gtggttgact caatggttca gcattttaaa gtaactatat ttggagaccg tagaccagtt	240
tatgatggaa aaagaagtct ttacaccgcc aatccacttc ctgtggcaac tacaggggta	300
gatttagacg ttactttacc tggggaagggt ggaaaagatc gacctttcaa ggtgtcaatc	360
aaatttgtct ctcggttgag ttggcaccta ctgcatgaag tactgacagg acggaccttg	420

cctgagccac	tggaattaga	caagccaatc	agcactaacc	ctgtccatgc	cgttgatgtg	480
gtgctacgac	atctgccctc	catgaaatac	acacctgtgg	ggcgttcatt	tttctccgct	540
ccagaaggat	atgaccaccc	tctggggagg	ggcagggaag	tgtggtttgg	attccatcag	600
tctgttcggc	ctgccatgtg	gaaaatgatg	cttaatatcg	atgtttctgc	cactgccttc	660
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gctgaaggaa	gtcacgtttc	aggacaaagc	aatgggcgag	atccacaagc	tcttgccaag	2520
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<220>  
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ggttccagtg	gaatacctgt gaaactgggt acaaacctct ttaacttaga ttttcccaa 180
gactggcagc	tataccagta ccatgtgaca tatattccag atttagcatc tagaaggctg 240
agaattgctt	tactttatag tcatagtga ctttccaaca aagcaaaagc attcgacggt 300
gccatccttt	ttctgtcaca aaagctagaa gaaaagggtca cagagttgtc aagtgaaact 360
caaagagggtg	agactataaa gatgactatc accctgaaga gggagctgcc atcaagttct 420
cccgtgtgca	tccagggtctt caatatcatc ttcagaaaga tcctcaaaaa gttgtccatg 480
taccaaattg	gacggaactt ctataatcct tcagagccaa tggaaattcc ccagcacaaa 540
ttatcccttt	ggcctggggt tgccatttct gtgtcatatt ttgaaaggaa gctcctgttt 600
agtgtgatg	tgagttacaa agtcctccgg aatgagacgg ttctggaatt catgactgct 660
ctctgtcaaa	gaactggctt gtcctgtttc acccagacgt gtgagaagca gctaataagg 720
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gtgaagccca	cacacacctt	tcagaagcgg	gatggcaccg	agatcaccta	tgtggattac	840
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ttaaagaaga	agagaaatga	caacagtgag	gctcagctcg	cccacctgat	acctgagctc	960
tgctttctaa	cagggctgac	tgaccaggca	acatctgatt	tccagctgat	gaaggctgtg	1020
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aacatccaga	ggaataccaa	tgctcgcttt	gaactagaga	cctggggact	gcatttttga	1140
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ccccacttg	gcactgttgt	ggattcagaa	gcaacacgta	acgaatggca	gtatgacttt	2040
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<210> 79  
<211> 2583



<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> HIWI, cDNA sequence of predicted ORF

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ccagcagagg gggaattatt tggccgtgga cggcagagag gaacagcagg aggaacagcc 180  
aagtcacaag gactccagat atctgctgga tttcaggagt tatcgttagc agagagagga 240  
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aaagaatcaa aaacagggttc ttcaggcatt atagtaaggt taagcactaa ccatttccgg 360  
ctgacatccc gtccccagtg ggccttatat cagtatcaca ttgactataa cccactgatg 420  
gaagccagaa gactccgttc agctcttctt tttcaacacg aagatctaata tggaaagtgc 480  
catgcttttg atggaacgat attattttta cctaaaagac tacagcaaaa ggttactgaa 540  
gttttttagta agacccggaa tggagaggat gtgaggataa cgatcacttt aacaaatgaa 600  
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ctc	2583

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 <213> Artificial Sequence

<220>  
 <223> Oligodeoxynucleotide with homology to human gene

<220>  
 <221> misc\_feature  
 <223> eIF2C1, primer (5'-3')

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<210> 81  
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<220>  
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<400> 81  
 cggtagaaga tgatgcgggt 20

<210> 82  
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<220>  
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<220>  
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 <223> eIF2C1, primer (5'-3')

<400> 82  
 gaggtctgta acattgtggc 20

<210> 83  
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<400> 83  
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<400> 84  
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<210> 85  
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<220>  
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<400> 85  
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<400> 86  
ccacaccagc gctctgcc

18

<210> 87  
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<213> Artificial Sequence

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<223> eIF2C1, primer (5'-3')

<400> 87

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18

<210> 88

<211> 20

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<223> eIF2C2, primer (5'-3')

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gaggtctgta acattgtggc

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<210> 89

<211> 20

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<223> eIF2C2, primer (5'-3')

<400> 89

cggtagaaga tgatgcgggt

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<210> 90

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<400> 94  
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<210> 95  
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<212> DNA  
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<220>  
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<223> eIF2C2, primer (5'-3')

<400> 95  
gatctcctgc cggtgctg

18

<210> 96  
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<212> DNA  
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<220>  
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<220>  
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<223> eIF2C3, primer (5'-3')

<400> 96  
agagcaacag tatgggtgggt ggac

24

<210> 97  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
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<220>  
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<400> 97  
tggatgtgtg atggtact

18

<210> 98  
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<223> eIF2C3, primer (5'-3')

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<210> 101

<211> 24

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<210> 102

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<223> eIF2C3, primer (5'-3')

<400> 102

agagcaacag tatggtgggt ggac

24

<210> 103

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<220>  
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<400> 103  
tcctggatga cctcttgact gtag

24

<210> 104  
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<220>  
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<223> eIF2C4, primer (5'-3')

<400> 104  
tccggcatct caagaacaca tattct

26

<210> 105  
<211> 26  
<212> DNA  
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<220>  
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<220>  
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<400> 105  
gaactcatat ggggtgtgtaa tgtctg

26

<210> 106  
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<220>  
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<220>  
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<223> eIF2C4, primer (5'-3')

<400> 106

atccaggact tggcctcc

18

<210> 107

<211> 26

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<223> eIF2C4, primer (5'-3')

<400> 107

gaactcatat ggggtgtgtaa tgtctg

26

<210> 108

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<223> Oligodeoxynucleotide with homology to human gene

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<223> HILI, primer (5'-3')

<400> 108

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18

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cggcctgaag gactgagacg tgt

23

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18

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